

RAW SEQUENCE LISTING

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Application Serial Number: 10/527,101
Source: PCF
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RAW SEQUENCE LISTING

DATE: 02/13/2006

PATENT APPLICATION: US/10/527,101

TIME: 13:10:11

Input Set : E:\Sequence Listing P1978R1.txt

Output Set: N:\CRF4\02132006\J527101.raw

```

3 <110> APPLICANT: SARAH C. BODARY
4     HILARY CLARK
5     JANET K. JACKMAN
6     JILL R. SCHOENFELD
7     WILLIAM I. WOOD
8     THOMAS D. WU
10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF PSORIASIS
12 <130> FILE REFERENCE: P1978R1-US
14 <140> CURRENT APPLICATION NUMBER: US 10/527,101
15 <141> CURRENT FILING DATE: 2005-03-09
17 <150> PRIOR APPLICATION NUMBER: PCT/US03/28362
18 <151> PRIOR FILING DATE: 2005-09-10
20 <150> PRIOR APPLICATION NUMBER: US 60/410,242
21 <151> PRIOR FILING DATE: 2002-09-11
23 <160> NUMBER OF SEQ ID NOS: 42
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 732
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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33 tgatggcttc atacatcgga tagttcccaa gttgatacaa aactggaaga 100
35 ttggccttat gtgcttcctg agtattatta ttactacagt ttgcattatt 150
37 atgatagcca catggtccaa gcatgctaaa cctgtggcat gttcagggga 200
39 ctggccttga gtgagagata agtgtttcta tttttctgat gataccagaa 250
41 attggacagc cagtaaaata tttttagtgg tgcagaaagc agaacttgct 300
43 cagattgata cacaagaaga catggaattt ttgaagaggt acgcaggaac 350
45 tgatatgcac tggattggac taagcaggaa acaaggagat tcttggaat 400
47 ggacaaatgg caccacattc aatggttggc catcaaactc caaatggtct 450
49 tgcaactgga gcctccgaca atggcttctt ctgctgggac cccttagata 500
51 ggcctctgag ggagctctga ctgccgtttc cccaaaacaa tgtcccctgt 550
53 cagcaggaag cagttaaatc agtcttcac cttatcctta atataacggc 600
55 agttagatgt acttctttag agggagtaaa tttatcaatt cagagcaatt 650
57 catcctcctc tttccatctt tgattcacag ttaataggct ataaattttg 700
59 ataattgtag ataaactaca gaaaacttct tg 732
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 160
63 <212> TYPE: PRT
64 <213> ORGANISM: Homo sapiens
66 <400> SEQUENCE: 2
67 Met Ile Asn Pro Glu Leu Arg Asp Gly Arg Ala Asp Gly Phe Ile
68   1           5           10           15
70 His Arg Ile Val Pro Lys Leu Ile Gln Asn Trp Lys Ile Gly Leu

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71          20          25          30
73 Met Cys Phe Leu Ser Ile Ile Ile Thr Thr Val Cys Ile Ile Met
74          35          40          45
76 Ile Ala Thr Trp Ser Lys His Ala Lys Pro Val Ala Cys Ser Gly
77          50          55          60
79 Asp Trp Leu Gly Val Arg Asp Lys Cys Phe Tyr Phe Ser Asp Asp
80          65          70          75
82 Thr Arg Asn Trp Thr Ala Ser Lys Ile Phe Cys Ser Leu Gln Lys
83          80          85          90
85 Ala Glu Leu Ala Gln Ile Asp Thr Gln Glu Asp Met Glu Phe Leu
86          95          100          105
88 Lys Arg Tyr Ala Gly Thr Asp Met His Trp Ile Gly Leu Ser Arg
89          110          115          120
91 Lys Gln Gly Asp Ser Trp Lys Trp Thr Asn Gly Thr Thr Phe Asn
92          125          130          135
94 Gly Trp Pro Ser Asn Ser Lys Trp Ser Cys Asn Trp Ser Leu Arg
95          140          145          150
97 Gln Trp Leu Leu Leu Leu Gly Pro Leu Arg
98          155          160
100 <210> SEQ ID NO: 3
101 <211> LENGTH: 2466
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
105 <400> SEQUENCE: 3
106 atctgtggga gcagtttatt ccagtatcac ccagggtgca gccacaccag 50
108 gactgtgttg aagggtgttt tttttctttt aaatgtaata cctcctcatc 100
110 ttttcttctt acacagtgtc tgagaacatt tacattatag ataagtagta 150
112 catggtggat aacttctact tttaggagga ctactctctt ctgacagtcc 200
114 tagactggtc ttctacacta agacaccatg aaggagtatg tgctcctatt 250
116 attcctggct ttgtgctctg ccaaaccctt ctttagccct tcacacatcg 300
118 cactgaagaa tatgatgctg aaggatatgg aagacacaga tgatgatgat 350
120 gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400
122 tccaacaaga gagccaagaa gccatttttt tccatttgat ctgtttccaa 450
124 tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500
126 ttaggtttga cctcagtcct aaccaacatt ccatttgata ctcgaatgct 550
128 tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gattttaaag 600
130 gactcacttc actttatggg ctgatcctga acaacaacaa gctaacgaag 650
132 attcacccaa aagcctttct aaccacaaag aagttgcgaa ggctgtatct 700
134 gtcccacaat caactaagtg aaataccact taatcttccc aaatcattag 750
136 cagaactcag aattcatgaa aataaagtta agaaaataca aaaggacaca 800
138 ttcaaaggaa tgaatgcttt acacgttttg gaaatgagtg caaaccctct 850
140 tgataataat gggatagagc caggggcatt tgaaggggtg acggtgttcc 900
142 atatcagaat tgcagaagca aaactgacct cagttcctaa aggcttacca 950
144 ccaactttat tggagcttca cttagattat aataaaaatt caacagtgga 1000
146 acttgaggat tttaaacgat acaaagaact acaaaggctg ggcctaggaa 1050
148 acaacaaaat cacagatatt gaaaatggga gtcttgctaa cataccacgt 1100
150 gtgagagaaa tacatttgga aaacaataaa ctaaaaaaa tcccttcagg 1150
152 attaccagag ttgaaatacc tccagataat cttccttcat tctaattcaa 1200
154 ttgcaagagt gggagttaat gacttctgtc caacagtgcc aaagatgaag 1250

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156 aaatctttat acagtgcaat aagttttattc aacaacccgg tgaaatactg 1300
158 ggaaatgcaa cctgcaacat ttcgttgtgt tttgagcaga atgagtgttc 1350
160 agcttgggaa ctttggaatg taataattag taattggtaa tgtccattta 1400
162 atataagatt caaaaatccc tacatttgga atacttgaac tctattaata 1450
164 atggtagtat tatatataca agcaaatatc tttctcaag tggttaagtcc 1500
166 actgacttat tttatgacaa gaaatttcaa cggaattttg ccaaaactatt 1550
168 gatacataag ggttgagaga aacaagcatc tattgcagtt tctttttgcg 1600
170 tacaaatgat cttacataaa tctcatgctt gaccattcct ttcttcataa 1650
172 caaaaaagta agatattcgg tatttaaacac tttgttatca agcacatttt 1700
174 aaaaagagct gtactgtaaa tggaatgctt gacttagcaa aatttgtgct 1750
176 ctttcatttg ctgtagaata aacagaatta acaaagacag taatgtgaag 1800
178 agtgcattac actattctta ttcttttagta gcttgggtag tactgttaata 1850
180 tttttaatca tcttaagta tgatttgata taatcttatt gaaattacct 1900
182 tatcatgtct tagagcccgt ctttatgttt aaaactaatt tcttaaaata 1950
184 aagccttcag taaatgttca ttaccaactt gataaatgct actcataaga 2000
186 gctggtttgg ggctatagca tatgcttttt tttttttaat tattacctga 2050
188 tttaaaaatc tctgtaaaaa cgtgtagtgt ttcataaaat ctgtaactcg 2100
190 cattttaatg atccgctatt ataagctttt aatagatga aaattgttag 2150
192 gctatataac attgccactt caactctaag gaataccttt gagatatccc 2200
194 tttggaagac cttgcttggg agagcctgga cactaacaat tctacaccaa 2250
196 attgtctctt caaatacgta tggactggat aactctgaga aacacatcta 2300
198 gtataactga ataagcagag catcaaatta aacagacaga aaccgaaagc 2350
200 tctatataaa tgctcagagt tctttatgta tttcttattg gcattcaaca 2400
202 tatgtaaaat cagaaaacag ggaaattttc attaaaaata ttgggttgaa 2450
204 aaaaaaaaaa aaaaaa 2466

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206 <210> SEQ ID NO: 4

207 <211> LENGTH: 381

208 <212> TYPE: PRT

209 <213> ORGANISM: Homo sapiens

211 <400> SEQUENCE: 4

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212 Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala
213 1 5 10 15
215 Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met
216 20 25 30
218 Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp
219 35 40 45
221 Asp Asp Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr
222 50 55 60
224 Arg Glu Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met
225 65 70 75
227 Cys Pro Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser
228 80 85 90
230 Asp Leu Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr
231 95 100 105
233 Arg Met Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu
234 110 115 120
236 Asn Asp Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn
237 125 130 135
239 Asn Asn Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr

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240		140		145		150
242	Lys Lys Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu					
243		155		160		165
245	Ile Pro Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His					
246		170		175		180
248	Glu Asn Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met					
249		185		190		195
251	Asn Ala Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn					
252		200		205		210
254	Asn Gly Ile Glu Pro Gly Ala Phe Glu Gly Val Thr Val Phe His					
255		215		220		225
257	Ile Arg Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu					
258		230		235		240
260	Pro Pro Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser					
261		245		250		255
263	Thr Val Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg					
264		260		265		270
266	Leu Gly Leu Gly Asn Asn Lys Ile Thr Asp Ile Glu Asn Gly Ser					
267		275		280		285
269	Leu Ala Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn					
270		290		295		300
272	Lys Leu Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu					
273		305		310		315
275	Gln Ile Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val					
276		320		325		330
278	Asn Asp Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr					
279		335		340		345
281	Ser Ala Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met					
282		350		355		360
284	Gln Pro Ala Thr Phe Arg Cys Val Leu Ser Arg Met Ser Val Gln					
285		365		370		375
287	Leu Gly Asn Phe Gly Met					
288		380				

290 <210> SEQ ID NO: 5

291 <211> LENGTH: 1082

292 <212> TYPE: DNA

293 <213> ORGANISM: Homo sapiens

295 <400> SEQUENCE: 5

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296 gatcccagac ctcggttgc agtagtgta gactgaagat aaagtaagtg 50
298 ctgtttgggc taacaggatc tcctcttgca gtctgcagcc caggacgctg 100
300 attccagcag cgccttaccg cgcagccga agattcacta tggtgaaaat 150
302 cgccttcaat acccctaccg ccgtgcaaaa ggaggaggcg cggcaagacg 200
304 tggaggccct cctgagccgc acggtcagaa ctcagatact gaccggcaag 250
306 gagctccgag ttgccacca ggaanaagag ggctcctctg ggagatgtat 300
308 gcttactctc ttaggccttt cattcatctt ggcaggactt attgttggtg 350
310 gagctgcat ttacaagtac ttcattgcca agagcaccat ttaccgtgga 400
312 gagatgtgct tttttgattc tgaggatcct gcaaattccc ttcgtggagg 450
314 agagcctaac ttcctgcctg tgactgagga ggctgacatt cgtgaggatg 500
316 acaacattgc aatcattgat gtgcctgtcc ccagtttctc tgatagtgac 550

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318 cctgcagcaa ttattcatga ctttgaaaag ggaatgactg cttacctgga 600
320 cttgttgctg gggaactgct atctgatgcc cctcaatact tctattgtta 650
322 tgcctccaaa aaatctggta gagctctttg gcaaactggc gaggggcaga 700
324 tatctgcctc aaacttatgt gggtcgagaa gacctagtgt ctgtggagga 750
326 aattcgtgat gtttagtaacc ttggcatctt tatttaccaa ctttgcaata 800
328 acagaaaagtc cttccgcctt cgtcgagag acctcttgct gggtttcaac 850
330 aaacgtgcca ttgataaatg ctggaagatt agacacttcc ccaacgaatt 900
332 tattgttgag accaagatct gtcaagagta agaggcaaca gatagagtgt 950
334 ccttggtaat aagaagtcag agatttacaa tatgacttta acattaaggt 1000
336 ttatgggata ctcaagatat ttactcatgc atttactcta ttgcttatgc 1050
338 cgtaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1082
340 <210> SEQ ID NO: 6
341 <211> LENGTH: 263
342 <212> TYPE: PRT
343 <213> ORGANISM: Homo sapiens
345 <400> SEQUENCE: 6
346 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
347 1 5 10 15
349 Glu Ala Arg Gln Asp Val Gln Ala Leu Leu Ser Arg Thr Val Arg
350 20 25 30
352 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
353 35 40 45
355 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu
356 50 55 60
358 Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr
359 65 70 75
361 Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys
362 80 85 90
364 Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
365 95 100 105
367 Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp
368 110 115 120
370 Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp
371 125 130 135
373 Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr
374 140 145 150
376 Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu
377 155 160 165
379 Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe
380 170 175 180
382 Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val
383 185 190 195
385 Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn
386 200 205 210
388 Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe
389 215 220 225
391 Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
392 230 235 240
394 Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile

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VERIFICATION SUMMARY

DATE: 02/13/2006

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Input Set : E:\Sequence Listing P1978R1.txt

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